



OIPE

ENTERED

600

660 720

780

840 900

960

1110

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/981,900B

DATE: 03/28/2002 PS

TIME: 16:29:17

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF3\03282002\I981900B.raw

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3 <110> APPLICANT: Sticklen, Masomeh B
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Magbool, Shahina B

Dale, Bruce E

7 <120> TITLE OF INVENTION: TRANSGENIC PLANTS CONTAINING LIGNINASE AND CELLULASE WHICH

DEGRADE LIGNIN

AND CELLULOSE TO FERMENTABLE SUGARS

- 10 <130> FILE REFERENCE: MSU 4.1-539
- 12 <140> CURRENT APPLICATION NUMBER: US/09/981,900B
- C--> 13 <141> CURRENT FILING DATE: 2002-03-18
 - 15 <150> PRIOR APPLICATION NUMBER: 60/242,408
 - 16 <151> PRIOR FILING DATE: 2000-10-20
 - 18 <160> NUMBER OF SEQ ID NOS: 22
 - 20 <170> SOFTWARE: PatentIn version 3.1
 - 22 <210> SEQ ID NO: 1
 - 23 <211> LENGTH: 1110
 - 24 <212> TYPE: DNA
 - 25 <213> ORGANISM: Oryza sativa
 - 27 <400> SEQUENCE: 1
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 - 32 coggectocg cggctcgage gccgtgccat ccgatccgct gagttttggc tatttatacg 180 240
 - 34 taccgcggga gcctgtgtgc agagagtgca tctcaagaag tactcgagca aagaaggaga 36 gagettggtg agetgeagag atggeeecet eegtgatgge gtegteggee accaeegteg 300
 - 38 ctcccttcca gggctcaagt ccaccgccgg catgccgtcg cccgccgtcc gaactccagc 360
 - 40 ttcggcaacg tcagcatggc ggcaggatca ggtgcatgca ggtaattacc tactgatcca 420
 - 42 acacacattc ttcttcttct tcttcttctt aaccaacatt aaccaacaac tcaattatcg 480

 - 44 tttattcatt gaggtgtggc cgattgaggg catcaagaag ttcgagaccc tctcctacct 540
 - 46 gccaccgctc accgtggagg acctcctgaa gcagatcgag tacctagctc cgttccaagt
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 - 56 cccgggctgc gaggagtctg gtggcaacta agccgtcatc gtcatatata gcctcgttta
 - 58 attgttcatc tctgattcga tgatgtctcc caccttgttt cgtgtgttcc cagtttgttt
 - 60 categietti tgattitaee ggeegigete igettitgit tittettite aceigatiet 1020 1080
 - 62 ctctctgact tgatgtaaga gtggtatctg ctacgactat atgttgtttg ggtgaggcat
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 - 67 <210> SEQ ID NO: 2
 - 68 <211> LENGTH: 38
 - 69 <212> TYPE: PRT
 - 70 <213> ORGANISM: Oryza sativa
 - 72 <400> SEQUENCE: 2
 - 74 Met Ala Pro Ser Val Met Ala Ser Ser Ala Thr Thr Val Ala Pro Phe
 - 5 10 75 1

Input Set : A:\PTO.VSK.txt

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87 <211> LENGTH: 6
88 <212> TYPE: PRT
89 <213> ORGANISM: Artificial Sequence
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92 <223> OTHER INFORMATION: Signal peptide targets the peroxisomes of plants
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102 <212> TYPE: DNA
103 <213> ORGANISM: Acidothermus cellulolyticus
105 <220> FEATURE:
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                                                                          180
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118 gccgaggcga tcccaatgag ggcaagggca agagcggagc cgatggcacg tcgggtggcc
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126 qacqcqatcq qqaqcaqqqc qqcqcqaqcc qqaccqtqtg gtcgaqccgg acqattcqcc
                                                                          540
128 catacogtoc tocaatoccc ageoccatot totcaatcco ccaaatocao caatocacac
                                                                          600
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132 cgcagagtag gcgactgtat gcggtaggtt ggcgctccag ccgtgggctg gacatgcctg
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138 acgggggaga acagacgggg gagaaaccaa cgggggattg gcg gtg ccg cgc gca
                                                     Val Pro Arg Ala
139
140
142 ttg cgg cga gtg cct ggc tcg cgg gtg atg ctg cgg gtc ggc gtc gtc
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143 Leu Arg Arg Val Pro Gly Ser Arg Val Met Leu Arg Val Gly Val Val
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                                            15
146 gtc gcg gtg ctg gca ttg gtt gcc gca ctc gcc aac cta gcc gtg ccg
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147 Val Ala Val Leu Ala Leu Val Ala Ala Leu Ala Asn Leu Ala Val Pro
148
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                                                                          979
150 cgg ccg gct cgc gcc gcg ggc ggc tat tgg cac acg agc ggc cgg
151 Arg Pro Ala Arg Ala Ala Gly Gly Gly Tyr Trp His Thr Ser Gly Arg
                40
                                    45
                                                                         1027
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155 Glu Ile Leu Asp Ala Asn Asn Val Pro Val Arg Ile Ala Gly Ile Asn
```

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Output Set: N:\CRF3\03282002\I981900B.raw

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	tgg	+++		++0	~ 22	200	taa		t 2.0	ata	ata	020		ata	taa	toa	1075
					-		_			_							10/3
	Trp		СТА	Pile	Gru	1111	75	ASII	тАт	vaı	vaı	80	GIY	ьeu	пр	261	
160		70															1122
	cgc																1123
	Arg	Asp	Tyr	Arg	Ser		ьeu	Asp	GIn	TTE	-	ser	Leu	GTÄ	туг		•
164						90					95					100	
	aca																1171
	Thr	Ile	Arg	Leu		Tyr	Ser	Asp	Asp		Leu	Lys	Pro	Gly		Met	
168					105					110					115		
	ccg		_					~	-		-	-	_	_		_	1219
171	Pro	Asn	Ser	Ile	Asn	Phe	Tyr	Gln	Met	Asn	Gln	Asp	Leu	Gln	Gly	Leu	
172				120					125					130			
174	acg	tcc	ttg	cag	gtc	atg	gac	aaa	atc	gtc	gcg	tac	gcc	ggt	cag	atc	1267
175	Thr	Ser	Leu	Gln	Val	Met	Asp	Lys	Ile	Val	Ala	Tyr	Ala	Gly	Gln	Ile	
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182	tcg	qcq	ctq	tqq	tac	acq	agc	agc	qtc	tcq	gag	gct	acq	tgg	att	tcc	1363
	Ser																
	165			-	•	170					175			-		180	
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	Asp																
188					185		V	5	-1-	190	1				195		
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	Gly																2103
192	O L y	1110	иор	200	1113	71011	Olu	110	205	1101	110	1114	CID	210	011	CID	
	ggc	aat	cca		atc	тас	taa	cas		acc	acc	σασ	caa		σσα	aac	1507
	Gly	-	_	_		_											1307
196	СТУ	тэр	215	261	116	тэр	115	220	пец	AIU	AIU	Giu	225	AIU	OLY	ASII	
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	Ala																1333
200	YIQ	230	пеп	ser	Val	ASII	235	HOII	пеп	цец	116	240	Val	Giu	Gry	AGT	
			+	224	~~~	~~~		+20	+~~	+ ~ ~	aaa		220	ata	~	993	1603
	cag																1003
	Gln	ser	туг	ASII	GLY	_	ser	Tyr	ттр	тгр		GTĀ	ASII	ьeu	GIII		
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	Ala	GTÀ	GIN	Tyr		vaı	vaı	Leu	Asn		Pro	Asn	Arg	Leu		Tyr	
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	gga																1795
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226 gtc cag tac cta cgg ccg acc gcg caa tac ggt gcg gac agc ttc cag 227 Val Gln Tyr Leu Arg Pro Thr Ala Gln Tyr Gly Ala Asp Ser Phe Gln 228 345 350 355 355 230 tgg acc ttc tgg tcc tgg aac ccc gat tcc ggc gac aca gga gga att 231 Trp Thr Phe Trp Ser Trp Asn Pro Asp Ser Gly Asp Thr Gly Gly Ile 232 360 365 370 234 ctc aag gtd gac tgg cag acg gtc gac aca gta aga ggc tat ctc 235 Leu Lys Asp Asp Trp Gln Thr Val Asp Thr Val Lys Asp Gly Tyr Leu 236 375 238 ggc ccg atc aag tcg tcg att tcc ggt ggc ggc ggc ggc tct gca tcg 239 Ala Pro Ile Lys Ser Ser Ile Phe Asp Pro Val Gly Ala Ser Ala Ser 240 390 395 400 242 cct agc agt caa ccg tcc ccg tcg gtg tcg ccg tct gcc gac gac 243 Pro Ser Ser Gln Pro Ser Pro Ser Val Ser Pro Ser Pro Ser Pro Ser 244 405 410 425 250 ccg acg cg agt cgg acg ccg acg ccd act ccg acg ccg acg ccg acg 251 Pro Thr Pro Thr Leu Thr Pro Thr Ala Thr Pro Thr Pro Thr Ala Ser 240 400 445 251 ccg acg ccg tca ccg acg gca acg gcc acg acg ccc acg gca acg 252 ry Gln Val Asn Ser Asp Trp Gly Asn Gly Phe Thr Val Ala 252 ry Gg gg acc aca gcg gcc acc acg acg acg gcg g		-	Thr	Thr	Leu	Gln		Thr	Thr	Asp	Gln		Trp	Leu	Lys	Thr		
227 val Gln Tyr Leu Arg Pro Thr Ala Gln Tyr Gly Ala Asp Ser Phe Gln 345 350 355 350 365 375 350 365 375 350 365 375 350 365 375 350 365 375 350 365 375 350 365 375 350 365 375 350 365 375 350 365 375 350 365 375 350 365 375 350 365 375 350 365 375 350 365 375 350 365 375 350 365 375 360 365			can	tac	cta	caa		acc	aca	саа	tac		aca	gac	age	ttc		1891
228																		1031
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231 Trp Thr Phe Trp Ser Trp Asn Pro Asp Ser Gly Asp Thr Gly Gly Ile 370 365 370 370 370 385 370 385		taa	acc	ttc	taa		taa	aac	CCC	αat		aac	gac	aca	ασа		att	1939
360																		
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235 Leu Lys Asp Asp Asp Trp Gln Thr Val Asp Thr Val Lys Asp Gly Tyr Leu 236 375 380 380 385 385 282 2838 geg ceg atc aag teg teg atc tet ceg geg ceg geg tet geg ceg teg ceg teg ceg ceg atc geg 2035 242 cet age agt caa ceg teg ceg ceg ceg geg ceg		ctc	ааσ	σat.		taa	caσ	acσ	atc		aca	gta	aaa	gac		tat	ctc	1987
236																		
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240																		
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243 Pro Ser Ser Gln Pro Ser Pro Ser Val Ser Pro Ser Pro Ser Pro Ser Ala Ser Aga deg ceg acg ceg acg cet act ceg acg ceg acg ceg acg cet act ceg acg acg ceg acg acg ceg acg acg acg ceg acg acg ceg acg acg ceg acg acg acg acg acg acg acg acg acg ac	242	cct	agc	agt	caa	ccg	tcc	ccg	tcg	gtg	tcg	ccg	tct	ccg	tcg	ccg	agc	2083
244 405 410 415 420 246 ccg tcg gcg agt cgg acg ccg acg ccg acg ccg acg ccg acg a																		
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248 425 430 435 250 ccg acg cca acg cct acg cct act gct acg ccc acg ccc acg gca agc 2179 251 Pro Thr Pro Thr Leu Thr Pro Thr Ala Thr Pro Thr Pro Thr Ala Ser 445 450 252 440 445 450 450 254 ccg acg ccg tca ccg acg gca gcc tcc gga gcc cgc tgc acc gcg agt 2227 255 Pro Thr Pro Ser Pro Thr Ala Ala Ser Gly Ala Arg Cys Thr Ala Ser 460 465 258 tac cag gtc acc agc gst tgg ggc at ggc tc acg ggt gcc 2275 259 Tyr Gln Val Asn Ser Asp Trp Gly Asn Gly Phe Thr Val Thr Val Ala 260 470 260 470 475 480 480 261 y gga aca at tcc gga tcc gtc gcg acc acg acg gtc agt ggc ggc ggg 2323 263 Val Thr Asn Ser Gly Ser Val Ala Thr Lys Thr Trp Thr Val Ser Trp 240 264 485 490 495 500 266 aca ttc ggc gga aat cag acg att acc aat tcg tgg aat gca gcg gtc gtc 2371 267 Thr Phe Gly Gly Asn Gln Thr Ile Thr Asn Ser Trp Asn Ala Ala Val 510 515 270 acg cag ac ggt cgg tcg gt acg gcg ccg cgg aat atg agt tc gcg ga tcg tcg gcg att gcg gcg cgg att gcg gcg gcg acg tcg tcg gcg	246	ccg	tcg	gcg	agt	cgg	acg	ccg	acg	cct	act	ccg	acg	ccg	aca	gcc	agc	2131
250 ccg acg cca acg ctg acc cct act gct acg ccc acg ccc acg gca agc 2179 251 Pro Thr Pro Thr Leu Thr Pro Thr Ala Thr Pro Thr Pro Thr Ala Ser 252	247	Pro	Ser	Ala	Ser	Arg	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Ala	Ser	
251 Pro Thr Pro Thr Leu Thr Pro Thr Ala Thr Pro Thr Pro Thr Ala Ser	248					425					430					435		
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256																		2227
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262 gtg aca aat tcc gga tcc gtc gcg acc aag aca tgg acg gtc agt tgg 2323 263 Val Thr Asn Ser Gly Ser Val Ala Thr Lys Thr Trp Thr Val Ser Trp 500 264 485 490 495 500 266 aca ttc ggc gga aat cag acg att acc aat tcg tgg aat gca gcg gtc 2371 267 Thr Phe Gly Gly Asn Gln Thr Ile Thr Asn Ser Trp Asn Ala Ala Val 515 515 270 acg cag aac ggt cag tcg gta acg gct cgg aat atg agt tat aac aac 2419 271 Thr Gln Asn Gly Gln Ser Val Thr Ala Arg Asn Met Ser Tyr Asn Asn 525 530 274 gtg att cag cct ggt cag aac acc acc acg ttc gga ttc cag gcg agc tat 2467 275 Val Ile Gln Pro Gly Gln Asn Thr Thr Phe Gly Phe Gln Ala Ser Tyr 545 278 acc gga agc aac gcg gca ccg aca gca gca				Val	Asn	Ser	Asp		Gly	Asn	Gly	Phe		Val	Thr	Val	Ala	
263 Val Thr Asn Ser Gly Ser Val Ala Thr Lys Thr Trp Thr Val Ser Trp 264 485																		0000
264 485 490 495 500 266 aca ttc ggc gga aat cag acg att acc aat tcg tgg aat gca gcg gtc 2371 267 Thr Phe Gly Gly Asn Gln Thr Ile Thr Asn Ser Trp Asn Ala Ala Val 505 510 515 270 acg cag aac ggt cag tcg gta acg gct cgg aat atg agt tat aac aac 2419 271 Thr Gln Asn Gly Gln Ser Val Thr Ala Arg Asn Met Ser Tyr Asn Asn 520 525 530 274 gtg att cag cct ggt cag aac acc acg ttc gga ttc cag agc tat 2467 275 Val Ile Gln Pro Gly Gln Asn Thr Thr Phe Gly Phe Gln Ala Ser Tyr 535 540 545 278 acc gga agc aac gcg gca ccg aca gtc gcc tgc gca gca agt taa 2512 279 Thr Gly Ser Asn Ala Ala Pro Thr Val Ala Cys Ala Ala Ser 250 555 282 tacgtcgggg agccgacggg agcggcggg agcgtccgga ccgtcggttc cccggcttcc acctatggag 2572 284 cgaacccaac aatccggacg gacctgcagg taccaggg taccaggg taccaggg taccaggag taccagaggg taccagag taccagagag gaacgacacg aatgcccacc 2632 286 atctcaaaac ggctgcagc cggcgtcctc gccggtcctc gccggggcgg taccagg taccagag taccagagag taccagagag taccagagag taccagagag taccagagag taccagagag taccagagag taccagagag taccagagagagaccagagaccagaaccagaaccagaaccagaaccaac																		2323
266 aca ttc ggc gga aat cag acg att acc aat tcg tgg aat gca gcg gtc 267 Thr Phe Gly Gly Asn Gln Thr Ile Thr Asn Ser Trp Asn Ala Ala Val 268 505 510 515 270 acg cag aac ggt cag tcg gta acg gct cgg aat atg agt tat aac aac 2419 271 Thr Gln Asn Gly Gln Ser Val Thr Ala Arg Asn Met Ser Tyr Asn Asn 272 520 525 530 274 gtg att cag cct ggt cag aac acc acg ttc gga ttc cag gcg agc tat 275 Val Ile Gln Pro Gly Gln Asn Thr Thr Phe Gly Phe Gln Ala Ser Tyr 276 535 540 545 278 acc gga agc aac gcg gca ccg aca gtc gcc tgc gca gca agt taa 279 Thr Gly Ser Asn Ala Ala Pro Thr Val Ala Cys Ala Ala Ser 280 550 555 560 282 tacgtcgggg agccgacggg agggtccgga ccgtcggttc cccggcttcc acctatggag 284 cgaacccaac aatccggacg gaactgcagg taccagagag gaacgacacg aatgccgcc 286 atctcaaaac ggctgcgagc cggcgtcctc gccggggcgg tgagcatcgc agcctccatc			Thr	Asn	Ser	Gly		Val	Ala	Thr	Lys		Trp	Thr	vaı	ser		
267 Thr Phe Gly Gly Asn Gln Thr Ile Thr Asn Ser Trp Asn Ala Ala Val 268																		2271
268 505 510 515 270 acg cag aac ggt cag tcg gta acg gct cgg aat atg agt tat aac aac 2419 271 Thr Gln Asn Gly Gln Ser Val Thr Ala Arg Asn Met Ser Tyr Asn Asn 272 520 525 530 274 gtg att cag cct ggt cag aac acc acg ttc gga ttc cag gcg agc tat 2467 275 Val Ile Gln Pro Gly Gln Asn Thr Thr Phe Gly Phe Gln Ala Ser Tyr 276 535 540 545 278 acc gga agc aac gcg gca ccg aca gtc gcc tgc gca gca agt taa 2512 279 Thr Gly Ser Asn Ala Ala Pro Thr Val Ala Cys Ala Ala Ser 280 550 555 560 282 tacgtcgggg agccgacggg agggtccga ccgtcggttc cccggcttcc acctatggag 2572 284 cgaacccaac aatccggacg gaactgcagg taccagagg gaacgacacg aatgcccgc 2632 286 atctcaaaac ggctgcgagc cggcgtcctc gccggggcgg tgagcatcgc agcctccatc																		23/1
270 acg cag aac ggt cag tcg gta acg gct cgg aat atg agt tat aac aac 2419 271 Thr Gln Asn Gly Gln Ser Val Thr Ala Arg Asn Met Ser Tyr Asn Asn 272 520 525 530 274 gtg att cag cct ggt cag aac acc acg ttc gga ttc cag gcg agc tat 2467 275 Val Ile Gln Pro Gly Gln Asn Thr Thr Phe Gly Phe Gln Ala Ser Tyr 276 535 540 545 278 acc gga agc aac gcg gca ccg aca gtc gcc tgc gca gca agt taa 2512 279 Thr Gly Ser Asn Ala Ala Pro Thr Val Ala Cys Ala Ala Ser 280 550 555 560 282 tacgtcgggg agccgacggg agggtccgga ccgtcggttc cccggcttcc acctatggag 2572 284 cgaacccaac aatccggacg gaactgcagg taccagagag gaacgacacg aatgcccgc 2632 286 atctcaaaac ggctgcgagc cggcgtcctc gccggggcgg tgagcatcgc agcctccatc		Thr	Pne	GIY	GLY		GIn	Thr	ше	THE		ser	ттр	ASII	Ата		Val	
Thr Gln Asn Gly Gln Ser Val Thr Ala Arg Asn Met Ser Tyr Asn Asn 520 530 The graph of the graph							.					+	- + -	20+	+-+		226	2410
525 530 274 gtg att cag cct ggt cag aac acc acg ttc gga ttc cag gcg agc tat 2467 275 Val Ile Gln Pro Gly Gln Asn Thr Thr Phe Gly Phe Gln Ala Ser Tyr 276 535 540 545 278 acc gga agc aac gcg gca ccg aca gtc gcc tgc gca gca agt taa 2512 279 Thr Gly Ser Asn Ala Ala Pro Thr Val Ala Cys Ala Ala Ser 280 550 555 560 282 tacgtcgggg agccgacggg agggtccgga ccgtcggtc cccggcttcc acctatggag 2572 284 cgaacccaac aatccggacg gaactgcagg taccagagg gaacgacacg aatgcccgc 2632 286 atctcaaaac ggctgcgagc cggcgtcctc gccggggcgg tgagcatcgc agcctccatc																		2413
274 gtg att cag cct ggt cag aac acc acg ttc gga ttc cag gcg agc tat 275 Val Ile Gln Pro Gly Gln Asn Thr Thr Phe Gly Phe Gln Ala Ser Tyr 276 535 540 545 278 acc gga agc aac gcg gca ccg aca gtc gcc tgc gca gca agt taa 2512 279 Thr Gly Ser Asn Ala Ala Pro Thr Val Ala Cys Ala Ala Ser 280 550 555 560 282 tacgtcgggg agccgacggg agggtccgga ccgtcggttc cccggcttcc acctatggag 2572 284 cgaacccaac aatccggacg gaactgcagg taccagagag gaacgacacg aatgcccgc 2632 286 atctcaaaac ggctgcgagc cggcgtcctc gccggggcgg tgagcatcgc agcctccatc		THE	GIII	ASII	_	GIII	ser	vaı	1111		ALG	ASII	Met	ser		ASII	ASII	
275 Val Ile Gln Pro Gly Gln Asn Thr Thr Phe Gly Phe Gln Ala Ser Tyr 276 535 540 545 278 acc gga agc aac gcg gca ccg aca gtc gcc tgc gca gca agt taa 2512 279 Thr Gly Ser Asn Ala Ala Pro Thr Val Ala Cys Ala Ala Ser 280 550 555 560 282 tacgtcgggg agccgacggg agggtccgga ccgtcggttc cccggcttcc acctatggag 2572 284 cgaacccaac aatccggacg gaactgcagg taccagagag gaacgacacg aatgcccgc 2632 286 atctcaaaac ggctgcgagc cggcgtcctc gccggggcgg tgagcatcgc agcctccatc 2692		ata	2++	a 2 a		aat	020	220	200		ttc	aas	ttc	car		age	tat	2467
276 535 540 545 278 acc gga agc aac gcg gca ccg aca gtc gcc tgc gca gca agt taa 2512 279 Thr Gly Ser Asn Ala Ala Pro Thr Val Ala Cys Ala Ala Ser 280 550 555 560 282 tacgtcgggg agccgacggg agggtccgga ccgtcggttc cccggcttcc acctatggag 2572 284 cgaacccaac aatccggacg gaactgcagg taccagagag gaacgacacg aatgcccgc 2632 286 atctcaaaac ggctgcgagc cggcgtcctc gccggggcgg tgagcatcgc agcctccatc 2692	274	y Ly ·	Tlo	Cln	Dro	99 C	Gln	aac	Thr	Thr	Dho	G1v	Dhe	Gln	Δla	Ser	Tur	2407
278 acc gga agc aac gcg gca ccg aca gtc gcc tgc gca gca agt taa 2512 279 Thr Gly Ser Asn Ala Ala Pro Thr Val Ala Cys Ala Ala Ser 280 550 555 560 282 tacgtcgggg agccgacggg agggtccgga ccgtcggttc cccggcttcc acctatggag 2572 284 cgaacccaac aatccggacg gaactgcagg taccagagag gaacgacacg aatgcccgc 2632 286 atctcaaaac ggctgcgagc cggcgtcctc gccggggcgg tgagcatcgc agcctccatc 2692		Vai	TTE		PIO	СТУ	GIII	ASII		1111	FIIC	GLY	rne		AIU	Der	1 7 1	
279 Thr Gly Ser Asn Ala Ala Pro Thr Val Ala Cys Ala Ala Ser 280 550 555 560 282 tacgtcgggg agccgacggg agggtccgga ccgtcggttc cccggcttcc acctatggag 2572 284 cgaacccaac aatccggacg gaactgcagg taccagagag gaacgacacg aatgcccgc 2632 286 atctcaaaac ggctgcgagc cggcgtcctc gccggggcgg tgagcatcgc agcctccatc 2692		acc	ααa		aac	aca	aca	cca		atc	αcc	tac	σса		aαt	taa		2512
280 550 555 560 282 tacgtcgggg agccgacggg agggtccgga ccgtcggttc cccggcttcc acctatggag 2572 284 cgaacccaac aatccggacg gaactgcagg taccagagag gaacgacacg aatgcccgcc 2632 286 atctcaaaac ggctgcgagc cggcgtcctc gccggggcgg tgagcatcgc agcctccatc 2692																		
282 tacgtcgggg agccgacggg agggtccgga ccgtcggttc cccggcttcc acctatggag 2572 284 cgaacccaac aatccggacg gaactgcagg taccagagag gaacgacacg aatgcccgcc 2632 286 atctcaaaac ggctgcgagc cggcgtcctc gccggggcgg tgagcatcgc agcctccatc 2692			-	J 0 1								-1-						
284 cgaacccaac aatccggacg gaactgcagg taccagagag gaacgacacg aatgcccgcc 2632 286 atctcaaaac ggctgcgagc cggcgtcctc gccggggcgg tgagcatcgc agcctccatc 2692				raa a	acco	acac	rg ac		ccaaa	a ccc	rtcad	ittc		gett	cc a	accta	atggag	2572
286 atctcaaaac ggctgcgagc cggcgtcctc gccggggcgg tgagcatcgc agcctccatc 2692																		
																2752		



Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF3\03282002\1981900B.raw

292 294 296 298 301 302	292 agaccaatge cactetegea gegaaaatge gegtegttte cacatatteg aeggeegtet 294 ggatggaceg categetgeg ateaaeggeg teaaeggegg acceggettg aegacatate 296 tggaegeege ceteteeeag cageagggaa ceaeceetga agteattgag attgteatet 296															2812 2872 2932 2992 3004	
304	<21	3> 0	RGAN:	ISM:		dothe	ermu	s ce.	llul	olyt	icus						
	<pre><400> SEQUENCE: 5 Val Pro Arg Ala Leu Arg Arg Val Pro Gly Ser Arg Val Met Leu Arg</pre>																
308		Pro	Arg	Ата	ьeu 5	Arg	Arg	Val	PIO	10	ser	Arg	Val	мес	ьеи 15	Arg	
		Glv	Val	Val	_	Ala	Val	Leu	Ala		Val	Ala	Ala	Leu	Ala	Asn	
313		1		20					25				-	30			
316	Leu	Ala	Val	Pro	Arg	Pro	Ala	Arg	Ala	Ala	Gly	Gly	Gly	Tyr	Trp	His	
317			35					40					45				
	Thr		Gly	Arg	Glu	Ile		Asp	Ala	Asn	Asn		Pro	Val	Arg	Ile	
321		50	_,	_	_	1	55	-1	-1	-1	~	60	~		1		
		GTA	тте	Asn	Trp		GTA	Phe	GIu	Thr	- •	Asn	Tyr	va⊥	Val		
325		T 0	m	Com	7 ~~	70	m	7 ~~	Com	Wot	75	7 an	Cln	тіс	T	80 Sor	
329	GTĀ	ьеи	пр	ser	85	ASP	TAT	AIG	ser	90	ьeu	ASP	GIII	ire	Lys 95	ser	
	Leu	Glv	Tur	Asn		Tle	Ara	Leu	Pro		Ser	Asp	Asp	Tle	Leu	Lvs	
333	пси	OI,	, + 1 -	100		110	**** 9	Deu	105	-1-	501	nop.	p	110	Leu	2,2	
	Pro	Gly	Thr		Pro	Asn	Ser	Ile	Asn	Phe	Tyr	Gln	Met	Asn	Gln	Asp	
337		*	115					120			-		125			-	
340	Leu	Gln	Gly	Leu	Thr	Ser	Leu	Gln	Val	Met	Asp	Lys	Ile	Val	Ala	Tyr	
341		130					135					140					
		Gly	Gln	Ile	Gly		Arg	Ile	Ile	Leu		Arg	His	Arg	Pro		
	145	_			_	150	_	_		_,	155	_		_	~1	160	
	Cys	Ser	Gly	GIn		Ala	Leu	Trp	Tyr		Ser	Ser	Vai	Ser	Glu	Ala	
349	mh∞	m-m	т1.	Cor	165	T OU	Cln	λla	T OU	170	Cln	λνα	Фил	Tvrc	175 Gly	λαη	
353	1111	пъ	ire	180	ASP	Leu	GIII	нта	185	мта	GIII	ALY	тут	190	СТУ	ASII	
	Pro	Thr	Val		Glv	Phe	Asp	Leu		Asn	Glu	Pro	His		Pro	Ala	
357			195		1			200					205				
	Cys	Trp		Cys	Gly	Asp	Pro		Ile	Asp	Trp	Arg	Leu	Ala	Ala	Glu	
361	_	210	_	_	_	_	215					220					
364	Arg	Ala	Gly	Asn	Ala	Val	Leu	Ser	Val	Asn	Pro	Asn	Leu	Leu	Ile	Phe	
365	225					230					235					240	
	Val	Glu	Gly	Val		Ser	Tyr	Asn	Gly	Asp	Ser	${ t Tyr}$	\mathtt{Trp}	\mathtt{Trp}	Gly	Gly	
369					245					250					255		
	Asn	Leu	GIn	_	Ala	GTA	Gln	Tyr		Val	Val	Leu	Asn.		Pro	Asn	
373 376	λνα	T O''	Val	260	Sor	λΊο	uic	λαν	265	λ 1 =	ሞኮኮ	Ser	₩a 1	270	Pro	Gln	
377	ALG	ьeu	275	тАт	Set	нта	птэ	280	тАт	ита	TILL	261	285	тЛт	FIO	GIII	
	Thr	Tro		Ser	Asp	Pro	Thr		Pro	Asn	Asn	Met		Glv	Íle	Trp	
381		290					295					300		1		L	
	Asn		Asn	Trp	Gly	Tyr	Leu	Phe	Asn	Gln	Asn	Ile	Ala	Pro	Val	Trp	



Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

DATE: 03/28/2002

PATENT APPLICATION: US/09/981,900B

TIME: 16:29:18

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF3\03282002\I981900B.raw

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date L:510 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 L:511 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 L:518 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 L:519 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 L:558 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 L:559 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 L:672 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 L:680 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 L:720 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7